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ID AX004614 standard; DNA; PRO; 327 BP.  
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 AC AX004614;  
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 SV AX004614.1  
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 DT 24-AUG-2000 (Rel. 64, Created)  
 DT 24-AUG-2000 (Rel. 64, Last updated, Version 1)  
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 DE Sequence 2 from Patent WO9915669.  
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 KW .  
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 OS Clostridium perfringens  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 XX  
 RN [1]  
 RA Gibert M., Popoff M.R.;  
 RT "Clostridium toxin, and method for preparing immunogenic compositions";  
 RL Patent number WO9915669-A/2, 01-APR-1999.  
 RL GIBERT MARYSE (FR);  
 RL PASTEUR INSTITUT (FR).  
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 FH Key Location/Qualifiers  
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 FT source 1..327  
 FT /db\_xref="taxon:1502"  
 FT /organism="Clostridium perfringens"  
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 DT 02-AUG-2001 (Rel. 68, Created)  
 DT 22-JAN-2002 (Rel. 70, Last updated, Version 3)  
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 DE Clostridium perfringens plasmid pCP13 DNA, complete sequence.  
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 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
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 OG Plasmid pCP13  
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 RN [1]  
 RP 1-54310  
 RA Shimizu T.;  
 RT ;  
 RL Submitted (12-APR-2001) to the EMBL/GenBank/DDBJ databases.  
 RL Tohru Shimizu, Institute of Basic Medical Sciences, University of Tsukuba,  
 RL Department of Microbiology; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305-8575,  
 RL Japan (E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,  
 RL Fax:81-298-53-3354)  
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 RN [2]  
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T.,  
 RA Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
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 DR SPTREMBL; Q93M84; Q93M84.  
 DR SPTREMBL; Q93M85; Q93M85.  
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 DR SPTREMBL; Q93M91; Q93M91.  
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 DR SWISS-PROT; Q93MD2; RES1\_CLOPE.  
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FT      AIKHTIKNTKKIEEEIIRCLKFVGLEGCKQNYIELSGGEQQRVAIARLMLKPSEIILA
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FT      pIP404 (166 aa); 25% identity in 156 aa overlap"
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FT      45% identity in 53 aa overlap"
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FT      SQNSLAMTLKTGVPGDKGTDFPGEWKRTMNNYLGANNYEISKSSYSYSDWRNRVKNSV
FT      IWTVDKGYAVIADTKQSPYGTKLHPNPNYIDDRGPGGKPTYHYIAITGYDDTPGNDRML
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FT      NEKISIPSISENLIVWSKSNNGYNLSSNIYMYDISKDSKILLSENNIIKPQIKNNII
FT      IATNIKDNSDFTESYLT KYDLKNSKWNFISNKSQVYNDVKNLSVDDPLIGENYISWWD
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FT      /note="61 aa, similar to gp:AF179847_5 putative resolvase
FT      from Lactococcus lactis (199 aa); 38% identity in 65 aa
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FT      /note="truncated"
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FT      RLGENRKETKELKLFL"
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FT      aa); 21% identity in 402 aa overlap"
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FT      KFSKAEGISAKDSIYRLADMFGIEPENNIDNSFKPSFHISNSDYKEIGIEPNRAMLN
FT      DINLERQSLAEVMELEKSCAKTMNELANDDKSTFLNINLNFKSMPIVYNNAKTYYS
FT      CIERINEYVKEYNSPIDGFNSLEVLLYKDFTKSLEELKLNKQIDILYRAGINERIGFDL
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FT      25943..27403
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FT      Bacillus anthracis (589 aa); 28% identity in 500 aa
FT      overlap"

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FT          KDKEKLLKEVKETTKEFIETIESSLLNIKEKEILIEDEAVKEFLGKDKVKINELSKKEL
FT          EELIEKNNSYTWFKIDENKEIDSKNFTGKNHVMVVKEDDSYRDIYVGKTYNLENLIYVD
FT          DNKNLYRLKKELEVEKTNNSEFFYKKNSEVLSMEYEKIDINLSSDKFISDENRELNEKGV
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FT          IINANIEVK"
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FT          overlap"
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FT      Bacillus anthracis (282 aa); 25% identity in 227 aa
FT      overlap"
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FT      LTFINKNNKTNEIKVKFYSDSRDISIDNNLKEQNKEGLTIELVNEEIEKVKKEIKDND
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FT      NKELNKIDKLNKKKEDLEKMKV"
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FT      protein homolog yvcE from Bacillus subtilis (473 aa); 47%
FT      identity in 168 aa overlap"
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FT      RKNLSDFRKKRLESIMLTIDNAIRNYGKLFDPGHSSIEDLTKEQIVSFEIRTLTGVDKRI
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FT      DYLINFEREARKYFGGLIFATQSIRDVVPDVSNSEVFEKIRTLFELTQYKFIMQQDNNNT
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FT      identity in 742 aa overlap"
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FT      Bacillus anthracis (222 aa); 23% identity in 222 aa
FT      overlap"
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FT      /note="709 aa, similar to gp:AF188935_14 pXO2-14 from
FT      Bacillus anthracis (952 aa); 21% identity in 798 aa
FT      overlap"
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